



human  
tez1  
EST2  
p123

Motif 0

AKFLHMLMSVYVVELLSRFFYVTETTTQKNR  
ISEIEWLVLGKRSNAKMLCLSDFEKQKQIFAEFIWLYNSFIIPILQSFYITESSDLNR  
LKDFRWLFISD--IWFTKHNFNENLNQLAICFISWLFRLIPKIIQTFFCYCTEISSVT-  
TREISWMQVET-SAKHFYFFDHEN-IYVLWKLRLWIFEDLVVSLIRCFFYVTEQQKSYSK  
\* . . . . . \* \* \*

human  
tez1  
EST2  
p123

Motif 1

LFFYRKSVWSKLQSIGIRQHILKRVQLRDVSEAEVVRQHREARPALLTSRLRFIPKP--DGL  
TVYFRKDIWKLRCRPI-TSMKMEAFKINENNVNMDTQK-TTLPAPAVIRLLPKK--NTF  
IVYFRHDTWNLITPFIYFKTYLVENNVCRNHSYTLS--NFNHSKMRIIPKKSNEF  
TYYYRKNIWDVIMKMSI-ADLKKETLAEVQKEVEEWKKS-LGFAPGKRLRLIPKK--TTF  
\* . . . . . \* \* \*

human  
tez1  
EST2  
p123

Motif 2

RPVNM DYVVGARTFRREKRAERLTSRVKALF-SVLNVERA  
RLITN-LRKRLIKMGSNKKMLVSTNQTLRPVASILKHLNEESSGIPFNLEVYMKLLTF  
RIIAIPCRGADEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKEF  
RPIMTFNKKIVNSDRKTTKLTNTKLNHLMLKTLKN-RMFKDPFGFAVFNDDVMKKY  
\* \* . . . . . \* \*

tez1  
EST2  
p123

Motif 3 (A)

KDILLKHRMFGR-KKYFVRIDIKSCYDRIKQDLMFRIVKK-KLKDPEFVIRKYATIHATS  
KQRLKKFNVLPELYFMKFDVKSCYDSIPRMECMRILKD-ALKNENGFFVRSQYFFNTN  
EEFVCKWKQVGQPKLFFATMDIEKCYDSVNREKLSFTFLTKTLSSDFWIMTAQIILKRKN  
\* . . . . . \* \* \*

FIG. 1

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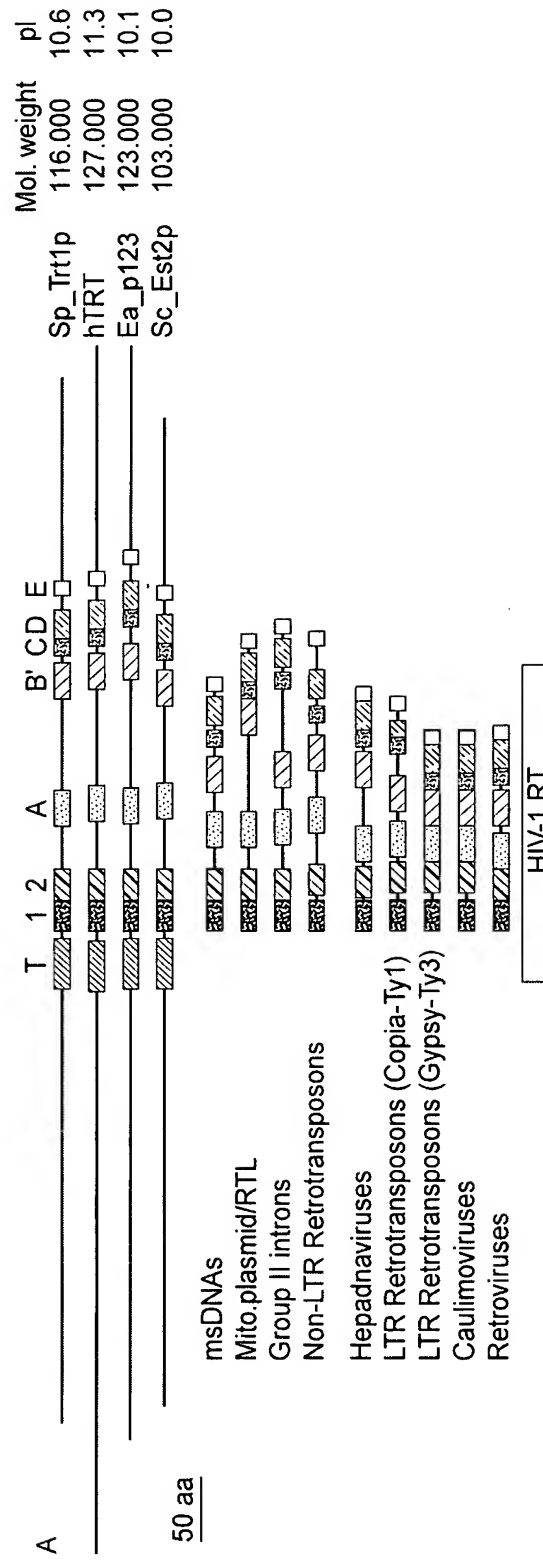


FIG. 2

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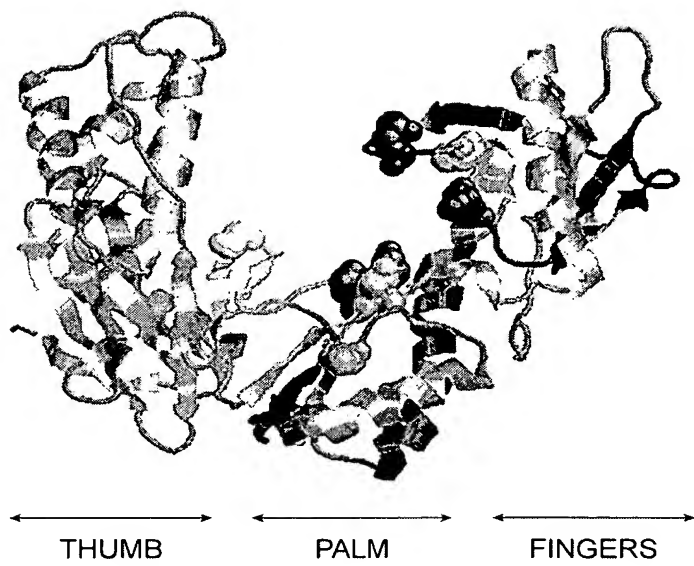


FIG. 3

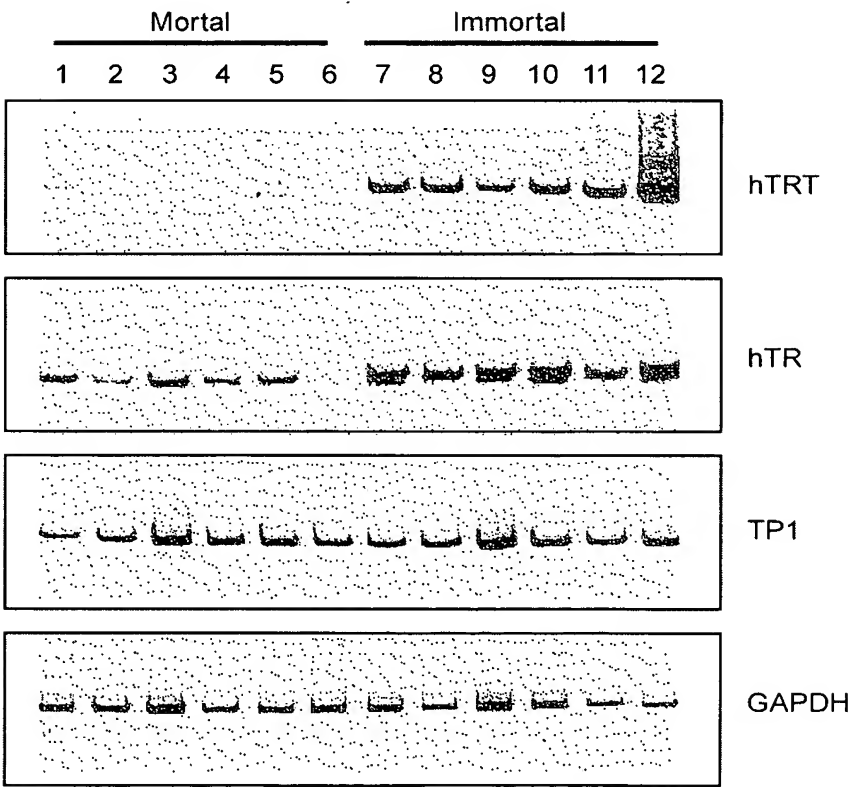


FIG. 5

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FIG. 4

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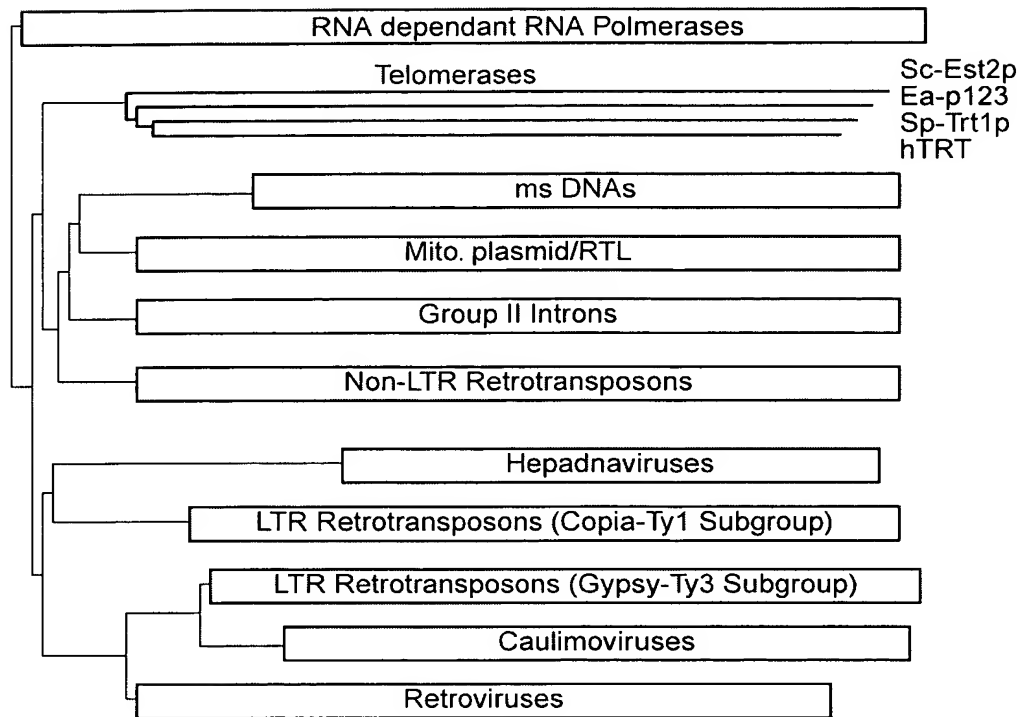


FIG. 6

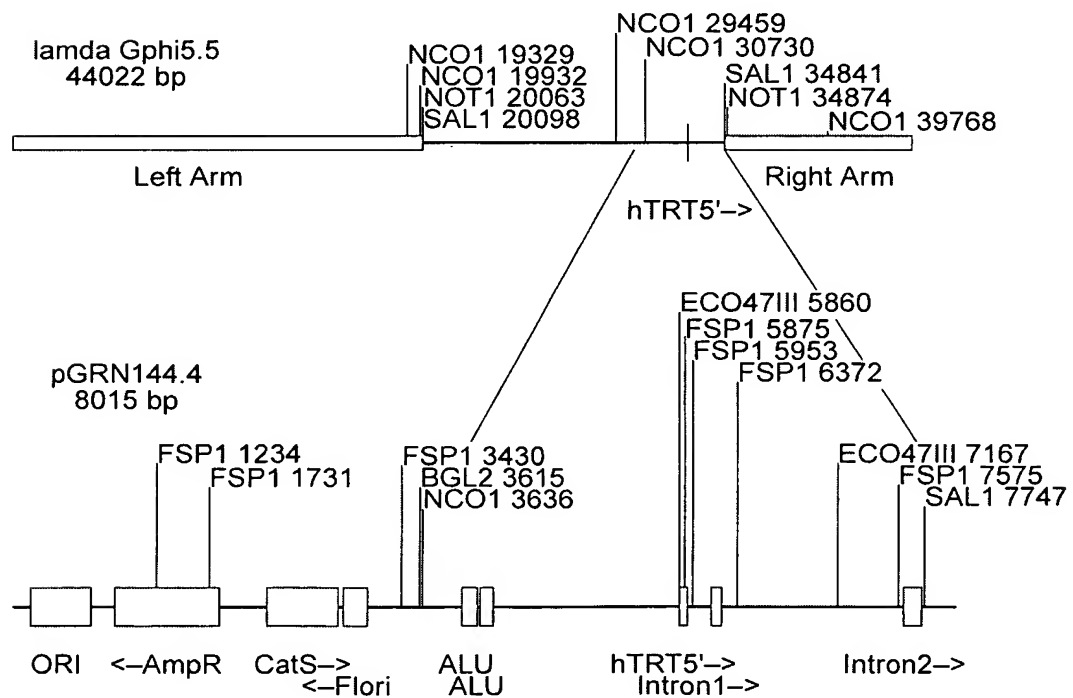


FIG. 7

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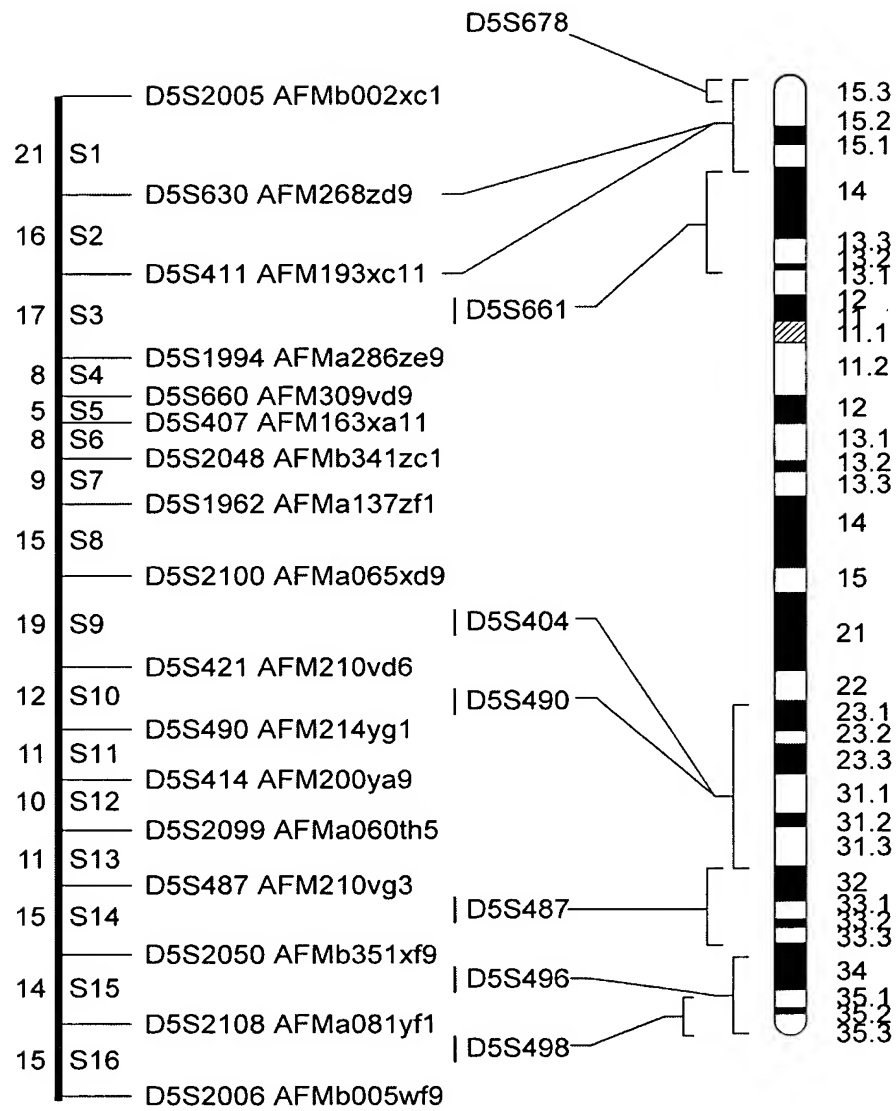


FIG. 8

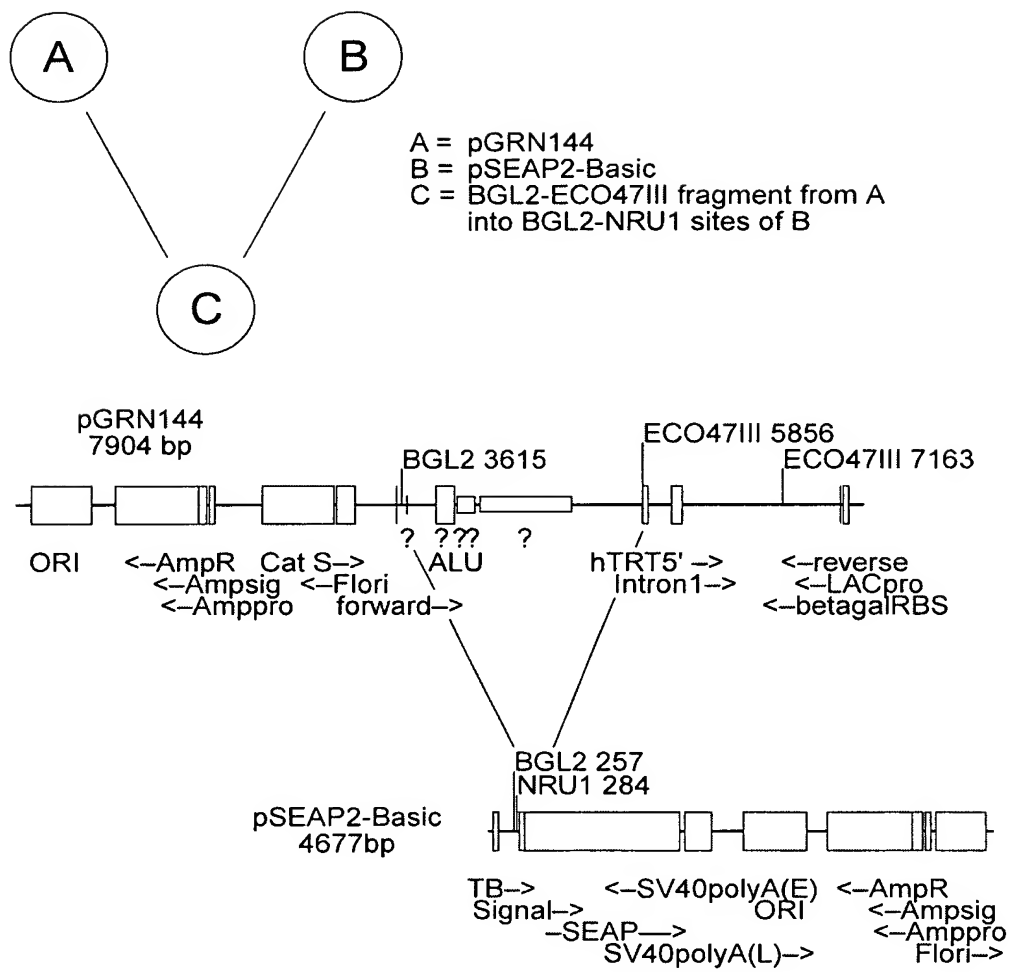


FIG. 9

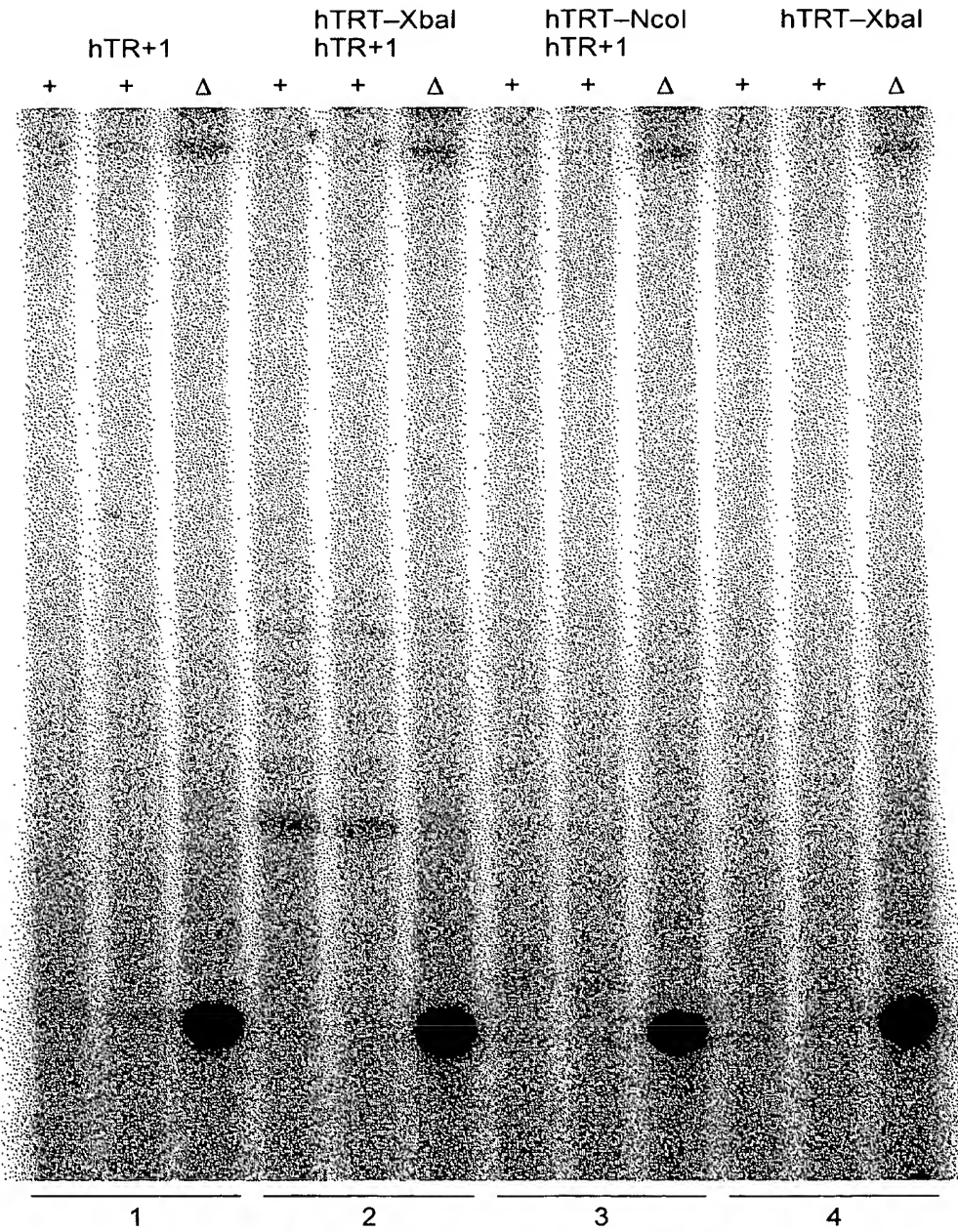


FIG. 10A



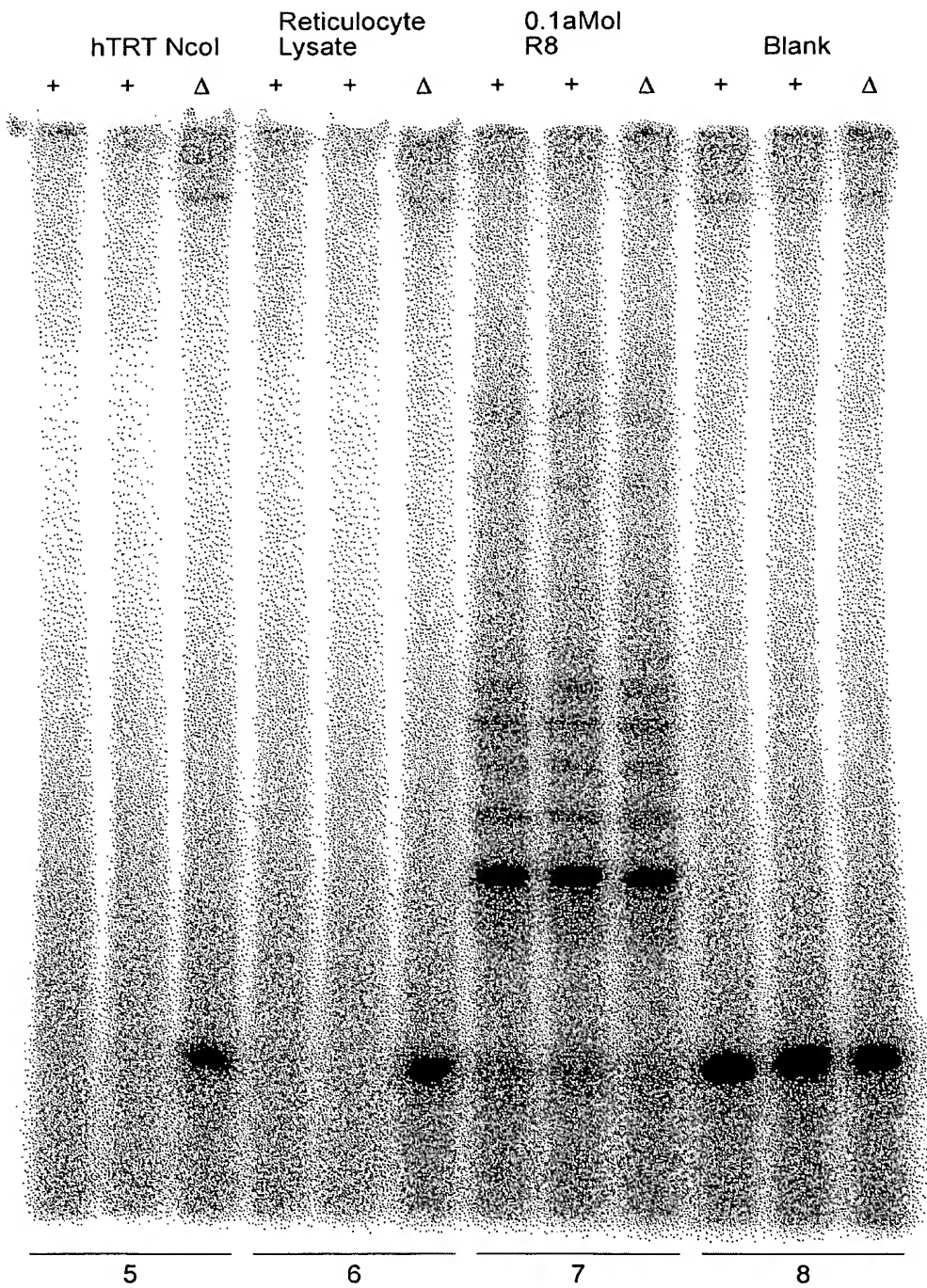


FIG. 10B

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Telomerase Specific Motifs

	MOTIF T	MOTIF T'
TRT con	W1	
hTRT	FFY TE	E V
spTRT	546 WLMSVYVVELLRSSFFVYVTTTFQKNRLFYRKSVWKLQSIGI	13 EAEVR
Ea_p123	429 WLYNSFIIPILQSFYITESSDLRNRVTYFRKDIWKLCPFI	12 ENNVR
Sc_Est2	441 WIFEDLVSLIRCFYVTEQQKSYSKTYYYRKNIDVIMKMSI	12 EKEVE
	366 WLFRLIPKIIQTFYCTEISSTVT.IVYFRHDTWNKLTTPFI	9 ENNVC

Telomerase RT Motifs (Fingers)

	MOTIF 1	MOTIF 2	MOTIF A	MOTIF B'
TRT con	R iPKk	fr I	p lyF D cYD i	Y q GIpQGs lS l Y
hTRT	11 SRLRFIPKPDG 0 LRPIV	69 PELYFVKVDVTGAYDTI	104 YVQCQGIPOGGSILSTLLCSLCY	
spTRT	10 AVIRLLPKKNT 0 FRLIT	66 RKKYFVRIDIKSCYDRI	99 YLQKVGIPQGSILSSFLCHFYM	
Ea_p123	10 GKRLIPKKT 0 FRPIM	67 PKLFFATMDIEKCYDSV	117 YKQTKGIPQGLCVSSILSSFFY	
Sc_Est2	13 SKMRIIPKKS 2 FRIIA	68 PELYFMKFDVKSCYDSI	85 YIREDEGLFQGSLSAPIVDLVY	
RT con	p hh h K	hR h	h hDh AF h	hPQG pP hh h
			GY	

Telomerase RT Motifs (Palm, Primer Grip)

	MOTIF C	MOTIF D	MOTIF E
TRT con	l1lrl DDfL it	g	n K w g s l
hTRT	15 LLLRLVDDFLVLT	15 GVPEYGCVVNLRKTVV	24 WCGLLLDTRTL
spTRT	16 VLLRVVDDFLFIT	15 GFEKHNFTSLEKTVI	22 FFGFSVNMRS
Ea_p123	24 LLMRLTDDYLLIT	15 VSRENGFKFNKKLQT	28 WIGISIDMKTL
Sc_Est2	18 LILKLADDFLIIS	15 GFQKYNAKANRDKILA	25 WKHSSTMNHF
RT con	h Y DDhh	Gh h cK h	hLG h
	F		

FIG. 11

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181 GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGC  
CCTGGGCCGCGCGAAAGGCGCGCGACCACCGGGTCACGGACCACACGCACGGGACCCTGCG

NFkB\_CS1  
GGGRQTYYQC  
NFkB-MHC-I.2  
TGGGCTTCCCC  
\*\*\*\*\*

241 ACGGCCGCCCCCGCCGCCCCCTCCTTCCGCCAGGTGGGCCTCCCCGGGGTCGGCGTCCG  
TGCCGGCGGGGGGCGGCGGGGAGGAAGGCGGTCCACCCGGAGGGGCCCCAGCCGCAGGC

Intron1  
\*\*\*\*\*

301 GCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTC  
CGACCCCAACTCCCGCCGGCCCCCCTTGGTCGCTGTACGCCTCTCGTCGCGTCCGCTGAG

NFkB\_CS1  
GGGRQTYYQC  
NFkB\_CS2  
RGGGRMTYYCC  
Topo\_II\_cleavage\_site  
RNYNNCNGYNGKTNYN  
\*\*\*\*\*>

361 AGGGCGCTTCCCCCGCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGG  
TCCCGCGAAGGGGGCGTCCACAGGACGGACTTCCTCGACCACCGGGCTCACGACGTCTCC

FIG. 12

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1   AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT
51  AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA
101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC
151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA
201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT
251 TTAGAAGATA TTAAATATTT TGCGCAGACA AATATTGTTG CTA CTCCACG
301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT
351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGA ACTTCTT
401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTC
451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA
501 CTCAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG
551 ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA
601 GCGAACTTCT GAAGGAACCTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG
651 ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA
701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA
751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA
801 ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT
851 AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTT
901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA
951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG
1001 CTTGAGAAAG TCAAAGATTT TAACCTCAAC TACTATTTAA CAAAATCTTG
1051 TCCTCTTCCA GAAAAATTGGC GGAACGGAA ACAAAAAATC GAAAACTTGA
1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC
1151 TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA
1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC
1251 AAAAGAAAGT TAAGAAATAT GTGGAACATA ACAAGCATGA ACTCATTCAC
1301 AAAA ACTTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA
1351 GGTTGAGACC TCTGCAAAGC ATTTTTATTA TTTTGATCAC GAAAACATCT
1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG
1451 CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA
1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA
1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT
1601 GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT
1651 ACCGAAGAAA ACTACTTTCC GTCCAATTAT GACTTTCAAT AAGAAGATTG
1701 TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC GAAGTTATTG
1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC
1801 TTTTGGATTG GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG
1851 AGTTTGTTTG CAAATGGAAG CAAGTTGGAC AACC AAAACT CTTCTTTGCA
1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAA ACTATC
1951 AACATTCCTA AAAACTACTA AATTACTTTC TTCAGATTTT TGGATTATGA
2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC
2051 TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAAGT
2101 TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG
2151 AACAAAATGA CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA
2201 AGAAATTTAT TTAAGAAAGA TAACCTACTT CAACCAGTCA TTAATATTTG
2251 CCAATATAAT TACATTA ACT TTAATGGGAA GTTTTATAAA CAAACAAAAG
2301 GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGT CATC ATTTTATTAT
2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA

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FIG. 13A

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2401 CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC
2451 TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT
2501 ATAAACGTAA GTCGTGAAAA TGGATTTAAA TTCAATATGA AGAAACTACA
2551 GACTAGTTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA
2601 GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC
2651 TCAATTGATA TGAAAACCTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT
2701 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT
2751 CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC
2801 CATTATTTTA GAAAGACGAT TACAACCGAA GACTTTGCGA ATAAACTCT
2851 CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG
2901 AATACAAGGA CCACTTTAAG AAGAAGCTAG CTATGAGCAG TATGATCGAC
2951 TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA
3001 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG
3051 ACTTTTTCCT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA
3101 AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCAA AAGAAGCAAA
3151 GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA
3201 CTATTCTAAC TTATTTTGGG AAGTTAATTT TCAATTTTGT TCTTATATAC
3251 TGGGGTTTTG GGGTTTTGGG GTTTTGGGG

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FIG. 13B

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1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHYKD
51 LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL
101 SSSDVSDRQK LQCFGFQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM
151 IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGG
201 ADMNEPRCCS TCKYNVKNK DHFLNNINVP NWNMKSRTTR IFYCTHFNRN
251 NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNRIRKKLK DKVIEKIAYM
301 LEKVKDFNFN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS
351 YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHELH
401 KNLLLEKINT REISWMQVET SAKHFYYFDH ENIYVLWKL RWIFEDLVVS
451 LIRCFFYVTE QQKSYSKTY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV
501 EEWKKS LGFA PGKLRLIPKK TFRPIMTFN KKIVNSDRKT TKLTTNTKLL
551 NSHMLKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA
601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVIDSKN
651 FRKKEMKD YF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKTLLIVEAKQ
701 RNYFKDNLL QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFY
751 ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVLFIKEL
801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI
851 SIDMKTLALM PNINLRIEGI LCTLNLNMQT KKASMWLKKK LKSFLMNNIT
901 HYFRKTITTE DFANKTLNKL FISGGYKYM CAKEYKDHFK KNLAMSSMID
951 LEVSKIIYSV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFI EIFSTK
1001 KYIFNRVCM I LKAKEAKLKS DQCQSLIQYD A

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FIG. 14

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1 ggtaccgatttacttcttcttcataagaactaattgcttctcctgaacgcctcctaaatctctggaaatatttttacaaga 80  
 81 actcaataacaataaccaggtcaaatcccaatgaaggtgtattagtgcagataaattctatttctatttctggtcgta 160  
 161 ccaagtataagacacaaagacaaacttctccccctaaagacttttacttatttaataatttacttttcaaatatatttcg 240  
 241 ggttcgcttacttttaactcggtgactgttttagctctactctagccaaacgcgtgtttctaccccgctcattggatat 320  
 321 agctctggagtagctcacagaaatccttcaaaatcttctgtagactatttagattacagtcggtgcataatc 400  
 401 ttaacatggagccttacactttagatgagtcagtcgcatgagtagtatttggatcatccaacggttgcccttgaaaaag 480  
 481 gttgataattattgcaaaatcatgctccttagtgggtgaatccgcgaaaagtgtttgatgcttgcacacgctagcatg 560  
 561 attgagatattcaaaaatttctatccactacaactcctttaacgcggtttatttttctatttctatctcatgttgtt 640  
 641 ccaaatatgtatcctcgtattaggctttttccggttttactcctggaatcgtaaccttttccactattccccctaatga 720  
 721 ataactaaattagtttcgcttataattgtagtagtaaaagattggtgattctactcgtgtaattgttagtttaa 800  
 801 gatactttgcaaaacatttattagctatcattatataaaaaaatccataattataaataatcaatatttgcggtc 880  
 881 actatttataaaacggttatgatcagtaggacactttgcataatatagttatgcttaagtacttgtaacttgc 958  
  
 959 atg acc gaa cac cat acc ccc aaa agc agg att ctt cgc ttt cta gag aat caa tat gta 1018  
 1 M T E H H T P K S R I L R F L E N Q Y V 20  
  
 1019 tac cta tgt acc tta aat gat tat gta caa ctt gtt ttg aga ggg tgc cgc gca agc tgc 1078  
 21 Y L C T L N D Y V Q L V L R G S P A S S 40  
  
 1079 tat agc aat ata tgc gaa cgc ttg aga agc gat gta caa acg tcc ttt tct att ttt ctt 1138  
 41 Y S N I C E R L R S D V Q T S F S I F L 60  
  
 1139 cat tgc act gta gtc ggc ttc gac agt aag cca gat gaa ggt gtt caa ttt tct tct cca 1198  
 61 H S T V V G F D S K P D E G V Q F S S P 80  
  
 1199 aaa tgc tca cag tca gag gtatatatatatttttggtttggatttttttctatttcgggatagctaataatgggcag 1272  
 81 K C S Q S E 86  
  
 1273 cta ata gcg aat gtt gta aaa cag atg ttc gat gaa agt ttt gag cgt cga agg aat cta 1332  
 87 L I A N V V K Q M F D E S F E R R N L 106  
  
 1333 ctg atg aaa ggg ttt tcc atg gtaaggatttctaattgtgaaatatttaccctgcaattactgtttcacaagaga 1405  
 107 L M K G F S M 113  
  
 1406 ttgtatttaaccgataaag aat cat gaa gat ttt cga gcc atg cat gta aac gga gta caa aat 1469  
 114 N H E D F R A M H V N G V Q N 128

FIG. 15A

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1470 GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA 1529  
 129 D L V S T F P N Y L I S I L E S K N W Q 148  
 1530 CTT TTG TTA GAA AT gtaaataccggttaagatgttggcactttgaacaagactgacaagtatag T ATC GGC 1601  
 149 L L L E I I G 155  
 1602 AGT GAT GCC ATG CAT TAC TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC 1661  
 156 S D A M H Y L L S K G S I F E A L P N D 175  
 1662 AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG 1721  
 176 N Y L Q I S G I P L F K N N V F E E T V 195  
 1722 TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA 1781  
 196 S K K R K R T I E T S I T Q N K S A R K 215  
 1782 GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT 1841  
 216 E V S W N S I S I S R F S I F Y R S S Y 235  
 1842 AAG AAG TTT AAG CAA G gtaactaatactgttatccttcataactaatttag AT CTA TAT TTT AAC 1907  
 236 K K F K Q D L Y F N 245  
 1908 TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG 1967  
 246 L H S I C D R N T V H M W L Q W I F P R 265  
 1968 CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA 2027  
 266 Q F G L I N A F Q V K Q L H K V I P L V 285  
 2028 TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA 2087  
 286 S Q S T V V P K R L L K V Y P L I E Q T 305  
 2088 GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT 2147  
 306 A K R L H R I S L S K V Y N H Y C P Y I 325  
 2148 GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG 2207  
 326 D T H D D E K I L S Y S L K P N Q V F A 345  
 2208 TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA 2267  
 346 F L R S I L V R V F P K L I I W G N Q R I 365

FIG. 15B

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2268 TTT GAG ATA ATA TTA AAA G gattgtataaaattattaccactaacgattttaccag AC CTC GAA ACT 2336  
 366 F E I I L K D L E T 375  
 2337 TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG 2396  
 376 F L K L S R Y E S F S L H Y L M S N I K 395  
 2397 gtaatatgccaaaattttttaccatttaataacaatcag ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA 2465  
 396 I S E I E W L V L G 405  
 2466 AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG 2525  
 406 K R S N A K M C L S D F E K R K Q I F A 425  
 2526 GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TTT TAT 2585  
 426 E F I Y W L Y N S F I I P I L Q S F F Y 445  
 2586 ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA 2645  
 446 I T E S S D L R N R T V Y F R K D I W K 465  
 2646 CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG 2705  
 466 L C R P F I T S M K M E A F E K I N E 485  
 2706 gtatttttaagtgatttttttgcacaaagctaataattttcag AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT 2775  
 486 N N V R M D T Q K T 495  
 2776 ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG 2835  
 496 T L P P A V I R L L P K K N T F R L I T 515  
 2836 AAT TTA AGA AAA AGA TTC TTA ATA AAG gtatttaatttttggtcatcaatgtactttacttctaattctatta 2906  
 516 N L R K R F L I K 524  
 2907 ttagcag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG 2967  
 525 M G S N K K M L V S T N Q T L R P V 542  
 2968 GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG 3027  
 543 A S I L K H L I N E S S G I P F N L E 562  
 3028 GTT TAC ATG AAG CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaat 3088  
 563 V Y M K L L T F K K D L L K H R M F G 581

FIG. 15C

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3089 tatataatgcgcgattcctcattattattgtcag G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA 3155  
 582 R K K Y F V R I D I 591  
 3156 AAA TCC TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG AAA CTC 3215  
 592 K S C Y D R I K Q D L M F R I V K K L 611  
 3216 AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT 3275  
 612 K D P E F V I R K Y A T I H A T S D R A 631  
 3276 ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaagtttatttttccattggaattttttaacaa 3343  
 632 T K N F V S E A F S Y F 643  
 3344 attcttttttttag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA 3405  
 644 D M V P F E K V V Q L L S M K T 659  
 3406 TCA GAT ACT TTG TTT GTT GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT 3465  
 660 S D T L F V D F V D Y W T K S S E I F 679  
 3466 AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT AAG gtataccaattgttgaattgtaataaca 3532  
 680 K M L K E H L S G H I V K 692  
 3533 ctaatgaaactag ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA 3593  
 693 I G N S Q Y L Q K V G I P Q G S 708  
 3594 ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG 3653  
 709 I L S S F L C H F Y M E D L I D E Y L S 728  
 3654 TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA 3713  
 729 F T K K K G S V L L R V V D D F L F I T 748  
 3714 GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gtgagttgctgcattcc 3777  
 749 V N K K D A K K F L N L S L R G 764  
 3778 taagttctaaccgttgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA 3840  
 765 F E K H N F S T S L E K T V 778  
 3841 ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA 3900  
 779 I N F E N S N G I I N N T F F N E S K K 798

FIG. 15D

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3901 AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT 3960
799 R M P F F G F S V N M R S L D T L L A C 818

3961 CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG 4020
819 P K I D E A L F N S T S V E L T K H M G 838

4021 AAA TCT TTT TTT TAC AAA ATT CTA AG gtatactgtgtaactgaataatagctgacaaataatcag A TCG 4089
839 K S F F Y K I L R S 848

4090 AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT 4149
849 S L A S F A Q V F I D I T H N S K F N S 868

4150 TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA 4209
869 C C N I Y R L G Y S M C M R A Q A Y L K 888

4210 AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtgagtacttattttaactaga 4274
889 R M K D I F I P Q R M F I T D 903

4275 aaagtcattaattaaccttag AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA AAG TTG GCC 4339
904 L L N V I G R K I W K K L A 917

4340 GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgtc 4401
918 E I L G Y T S R R F L S S A E V K W 935

4402 ggtctcgagacttcagcaaatattgacacatcag G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA 4468
936 L F C L G M R D G L K 946

4469 CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT 4528
947 P S F K Y H P C F E Q L I Y Q F Q S L T 966

4529 GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA ATA 4588
967 D L I K P L R P V L R Q V L F L H R R I 986

4589 GCT GAT TAA tgtcatttttcaatttattattacatccctttattactgggtgtcttaaacaaatattattactaagtata 4665
987 A D * 989

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FIG. 15E

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4666 gctgacccccaaagcaagcatactataggatttctagtaaaagtaaaataatctcgttattagttttgattgacttgtct 4745  
4746 ttatccttataacttttaagaaagattgacagtgttgtagtactgcccacatgcccattaaacgggagtggttaaaca 4825  
4826 ttaaaagtaatacatgaggctaatactcctttcatttagaataaggaaagtgggttttctataatgaataatgccgcacta 4905  
4906 atgcaaaaagacgaagattatcttcaacaaggggattaaagcatatccgaaggaaagagagtaatatataccagtggt 4985  
4986 gttgaagaaagcaaggataatttggaacaagcttctgcagatgacaggctaataatttggtgaccgaattttggtaaaagc 5065  
5066 cccaggttatccatggtggccgacctgctactgagacgaaaagaaactaaggatagtttgaataactaatagctcattta 5145  
5146 atgtcttataaaggtttgtttttcctgacttcaattttgcatgggtgaaaagaaatagtgttaagccattattggat 5225  
5226 tccgaaatagccaaatttcttggttcctcaaacggaagtcctaaagaacttattgaagcttatgaggttcaaaaactcc 5305  
5306 tcctgatttaaggaggaatcttccacgatgaggaatggatagcttatcagctgctgaggagagaagcctaattttttgc 5385  
5386 aaaaaagaaatatcatgggagacatctcttgatgaatcagatcggagagtatctccagcggatccttgatgtcaata 5465  
5466 acttctatttctgaaatglatggtcctactgctcgacttctcgtagctctacgcagtttaagtgaaccaaaagggtacc 5544

FIG. 15F

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1 gcagcgctgc gtccctgctgc gcacgtggga agccctggcc ccggccaccc ccgcgatgcc
61 ggcgcgtccc cgctgccgag ccgtgcgctc cctgctgcgc agccactacc gcgaggtgct
121 gccgctggcc acgttcgtgc ggcgcctggg gccccagggc tggcggtggc tgcagcgctg
181 ggaccccgcg gctttccgcg cgctgggtgg ccagtgcctg gtgtgcgtgc cctggggacgc
241 agggccgccc cccgcccgcc cctccttcgg ccaggtgtcc tgcctgaagg agctggtggc
301 ccgagtgctg cagaggctgt gcgagcgctg ccgaagaac gtgctggcct tccggttcgc
361 gctgctggac ggggcccgcg ggggcccccc cgaggccttc accaccagcg tgcgcagcta
421 cctgcccac acggtgaccg acgcactgcg ggggagcggg gcgtggggggc tgctgctgcg
481 ccgctggggc gacgacgtgc tggttcacct gctggcacgc tgcgcgtctc ttgtgctggt
541 ggctcccagc tgcgcctacc aggtgtgcgg gccgcgctg taccagctcg gcgctgccac
601 tcaggcccg ccccgccac acgctagtgg acccggaagg cgtctgggat gcgaacgggc
661 ctggaacct agcgtcaggg aggcgggggt cccctgggc ctgccagccc cgggtgcgag
721 gaggcgctgg ggcagtgcga gccgaagtct gccgttgccc aagaggccca ggcgtggcgc
781 tgcccctgag ccggagcgga cgcctgtgg gtcaggggtcc tgggcccacc cgggcaggac
841 gcgtggaccg agtgaccgtg gtttctgtgt ggtgtcacct gccagaccgc ccgaagaagc
901 caccctcttt gaggggtgcg tctctggcac gcgccactcc caccatccg tgggcccga
961 gcaccagcg ggcctccat ccacatcgcg gccaccacgt ccttgggaca cgccttgtcc
1021 cccggtgtac gccgagacca agcacttctc tactcctca ggcgacaagg ggcgctcgcg
1081 gccctccttc ctactcagct ctctgaggcc cagcctgact ggcgctcgga ggctcgtgga
1141 gaccatcttt ctgggttcca ggccctggat gccagggact ccccgagggt tgcctcgctc
1201 gccccagcgc tactggcaaa tgcggccctc gtttctggag ctgcttggga accaccgcga
1261 gtgccccctac ggggtgctcc tcaagacgca ctgcccgcgt cgagctgcgg tcaccaccgc
1321 agccggtgtc tgtgcccggg agaagcccca gggctctgtg gcggcccccg agggaggaga
1381 ccagaccccc cgctgcctgg tgcagctgct ccgccagcac agcagccctc ggcaggtgta
1441 cagcttcgtg cgggcctgcc tgcgcgggt gggtcccca ggctctggg gccccaggca
1501 caacgaacgc cgcttctca ggaacaccaa gaagttcatc tccctgggga agcatgccaa
1561 gctctcgctg caggagctga cgtggaagat gagcgtgcgg gactgcgctt ggctgcgcag
1621 gagcccaggg gttggctgtg ttccggccgc agagcaccgt ctgctgagg agatcctggc
1681 caagtctctg cactggctga tgagtgtgt cgtcgtcgag ctgctcagg ctttctttta
1741 tgtcacggag accacgtttc aaaagaacag gctctttttc taccggaaga gtgtctggag
1801 caagttgcaa agcattggaa tcagacagca cttgaagagg gtgcagctgc gggagctgtc
1861 ggaagcagag gtcaggcagc atcggaagc caggcccgcc ctgctcaag ctgactccg
1921 cttcatcccc aagcctgacg ggctgcggcc gatgtgaac atggactacg tgcgtggagc
1981 cagaacgttc cgcagagaaa agagggccga gcgtctcacc tcgaggggtg aggcactgtt
2041 cagcgtgctc aactacgagc gggcgcgggc ccccgccctc ctgggcgctc ctgtgctggg
2101 cctggacgat atccacaggg cctggcgcac ctctgtgctg cgtgtgcggg cccaggacct
2161 gccgcctgag ctgtactttg tcaaggtgga tgtgacgggc gcgtacgaca ccatcccca
2221 ggacaggtc acggaggtca tcgccagcat catcaaacc cagaacacgt actgcgtgcg
2281 tcggtatgcc gtggtccaga aggcgcctcc tgggcacgtc cgcaaggcct cgaagccca
2341 cgtctctacc ttgacagacc tccagccgta catgagacag ttcgtggctc acctgcagga
2401 gaccagcccg ctgagggatg ccgtcgtcat cgagcagagc tccctccctga atgaggccag
2461 cagtggcctc ttgacgtct tctacgctt catgtgccac cagcgcgtgc gcactcaggg
2521 caagtccctac gtccagtgcc aggggatccc caggggctcc atcctctcca cgtgctctg
2581 cagcctgtgc tacggcgaca tggagaacaa gctgtttgcg gggattcggc gggacgggct
2641 gctctgcgtg ttgggtggat atttcttgtt ggtgacacct cactcacc cgcgaaaaac
2701 cttcctcagg accctggctc gaggtgtccc tgagtatggc tgcgtgggtg actgctggaa
2761 gacagtgggt aacttccctg tagaagacga ggccctgggt ggcacggctt ttgttcagat
2821 gccggccccc ggccatttcc cctggtgcgg cctgctgctg gatacccggg ccctggaggt
2881 gcagagcgac tactccagct atgccggac ctccatcaga gccagtctca ccttcaaccg
2941 cggcttcaag gctgggagga acatggcgct caaactcttt ggggtcttgc ggctgaagtg
3001 tcacagcctg tttctggatt tgcaggtgaa cagcctccag acggtgtgca ccaacatcta
3061 caagatcctc ctgctgcagg cgtacaggtt tcacgcaggt gtgctgcagc tcccatttca
3121 tcagcaagtt tggaagaacc ccacattttt cctgcgcgtc atctctgaca cggcctccct
3181 ctgctactcc atcctgaaag ccaagaacgc agggatgtcg ctgggggcca agggcgccgc
3241 cgccctctcg cctccgagg ccgtgcagtg gctgtgccac caagcattcc tgctcaagct
3301 gactcgacac cgtgtcacct acgtgccact cctggggtca ctcaggacag ccagacgca
3361 gctgagtcgg aagctcccg ggacgacgct gactgccctg gagggccgag ccaaccggc
3421 actgccctca gacttcaaga ccacctgga ctgatggcca cccgccaca gccaggccga
3481 gagcagacac cagcagccct gtcacgcgg gctctacgtc ccagggaggg aggggcccgc
3541 cacaccagg cccgacccg tgggagctcg aggcctgagt cagtggttgg ccgagggcctg
3601 catgtccggc tgaaggctga gtgtccggct gaggcctgag cgagtgtcca gccaagggtc
3661 gagtgtccag cacacctgcc gtcttctact cccacaggc tggcgctcgg ctccaccca
3721 gggcgagctt ttccctacca ggagccggc ttccactccc cacataggaa tagtccatcc
3781 ccagattcgc cattgttcac gccctccttt gccctccacc cccaccatcc cccaccatcc
3841 aggtggagac cctgagaagg accctgggag ctctgggaat ttggagtgac caaaggtgtg
3901 cctgtacac cctgcacctg cctgcacctg gatgggggtc cctgtgggtc aaattggggg
3961 gaggtgctgt gggagtaaaa tactgaatat atgagttttt cagttttgaa aaaaa

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FIG. 16

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MPRAPRCRAVRSLLRSHYREVLPLATFVRRRLGPQGWRLVQRGDP  
 AAFRALVAQCLVCVPWDARPPPAAPSFRQVSCLELVARVLQRL  
 CERGAKNVLAFGFALLDGARGGPPEAFTTSVRSYLPNTVTDALR  
 GSGAWGLLLRRVGDVVLVHLLARCALFVLVAPSCAYQVCGPPLY  
 QLGAATQARPPPHASGPRRRRLGCERAWNHSVREAGVPLGLPAPG  
 ARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRG  
 PSDRGFCVVSAPPAEEATSLEGALSGTRHSHPSVGRQHHAGPP  
 STSRPPRPWDTPCPPVYAETKHFYSSGDKEQLRPSFLLSSLRP  
 SLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLEL  
 LGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPGGSVAAPPEE  
 EDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGSRHNE  
 RRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGC  
 VPAAEHLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNR  
 LFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAQVROHREARPA  
 LTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA  
 LFSVLNYERARRPGLLGASVGLGLDDIHRWRTFVLRVRAQDPPP  
 ELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQ  
 KAAHGHVRKAFKSHVSTLTDLPYMRQFVAHLQETSPLRDVVI  
 EQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPOGSI  
 LSTLLCSLCYGD MENKLFAGIRRDGLLLRLVDDFLLVTPHLTHA  
 KTFRLTLVRGVPEYGCVVNLKRTVNFVVEDEALGGTAFVQMPA  
 HGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGR  
 NMRRKLFGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRF  
 HACVLQLPFHQVWKNPTFFLRVISDTASLCYSILKAKNAGMSL  
 GAKGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQ  
 TQLSRKLPGTTLTALEAAANPALPSDFKTILD

FIG. 17

GGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTT  
 TTATGTCACGGAGACCACGTTTCAAAGAAGCAGGCTCTTTTCTACCGGAAGAGTGTCTG  
 GAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTGAAGAGGGTGACGTGCGGGAGCT  
 GTCGGAAGCAGAGGTACGGCAGCATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGACT  
 CCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTGCTGGG  
 AGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACT  
 GTTCAGCGTGCTCAACTACGAGCGGGCGCGGCCCGCCCTCTGGGCGCCTCTGTGCT  
 GGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGCTGCGGGCCAGGA  
 CCGCGCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCC  
 CCAGGACAGGCTACGGAGGTATCGCCAGCATCATCAAACCCAGAACACGTACTGCGT  
 GCGTCGGTATGCCGTGGTCCAGAAGGCCGCCATGGGCACGTCCGCAAGGCCTTCAAGAG  
 CCACGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCT  
 GCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTGCGGGGATTGCGCGGGACGGGC  
 TGCTCCTGCGTTTGGTGGATGATTTCTGTTGGTGACACCTCACCTCACCCACGCGAAAA  
 CCTTCTCAGGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTTGCAG  
 AGACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCAGGCTTTGTTGAGA  
 TGCCGGCCACGGCCTATTTCCCTGGTGGCGCTGCTGCTGGATACCCGACCTGGAGG  
 TGCAGAGCGACTACTCCAGCTATGCCCGACCTCCATCAGAGCCAGTCTCACCTTCAACC  
 GCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGGCGCTGAAGT  
 GTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCCACCAACATCT  
 ACAAGATCCTCCTGCTGCAGGCGTACAGGTTTACGCATGTGTGCTGCAGCTCCCATTTC  
 ATCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCATCTCTGACACGGCCTCCC  
 TCTGCTACTCCATCTGAAAGCCAAGACGAGGGATGTGCTGGGGGCCAAGGGCGCCG  
 CCGGCC7TCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGC  
 TGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAGACGC  
 AGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGAGCCAACCCGG  
 CACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCCG  
 AGACAGACACAGCAGCCCTGTACGCCCGGCTCTACGTCCCAGGGAGGGGGCGGC  
 CCACACCCAGGCCGTGACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTGTTGGCCGAGGCCT  
 GCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGC  
 TGAGTGTCCAGCACACCTGCCGTCTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCC  
 AGGGCCAGCTTTTCTCACAGGAGGCCGCTTCCACTCCCCACATAGGAATAGTCCATC  
 CCCAGATTGCGCATTGTTACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCCACCATC  
 CAGGTGGAGACCTGAGAAGGACCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGT  
 GCCCTGTACACAGGCGAGGACCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGG  
 GGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTGTG0AAAAAAAAA  
 AAAAAAAAAAAAAAAAAA

FIG. 18

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MetSerValTyrValValGluLeuLeuArgSerPhePhe  
 TyrValThrGluThrThrPheGlnLysAsnArgLeuPhe  
 PheTyrArgLysSerValTrpSerLysLeuGlnSerIle  
 GlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu  
 LeuSerGluAlaGluValArgGlnHisArgGluAlaArg  
 ProAlaLeuLeuThrSerArgLeuArgPheIleProLys  
 ProAspGlyLeuArgProIleValAsnMetAspTyrVal  
 ValGlyAlaArgThrPheArgArgGluLysArgAlaGlu  
 ArgLeuThrSerArgValLysAlaLeuPheSerValLeu  
 AsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAla  
 SerValLeuGlyLeuAspAspIleHisArgAlaTrpArg  
 ThrPheValLeuArgValArgAlaGlnAspProProPro  
 GluLeuTyrPheValLysValAspValThrGlyAlaTyr  
 AspThrIleProGlnAspArgLeuThrGluValIleAla  
 SerIleIleLysProGlnAsnThrTyrCysValArgArg  
 TyrAlaValValGlnLysAlaAlaHisGlyHisValArg  
 LysAlaPheLysSerHisValLeuArgProValProGly  
 AspProAlaGlyLeuHisProLeuHisAlaAlaLeuGln  
 ProValLeuArgArgHisGlyGluGlnAlaValCysGly  
 AspSerAlaGlyArgAlaAlaProAlaPheGlyGly

FIG. 19

1  
met

GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

10

pro arg ala pro arg cys arg ala val arg ser leu leu arg ser  
 CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

20

his tyr arg glu val leu pro leu ala thr phe val arg arg leu  
 CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

30

40

gly pro gln gly trp arg leu val gln arg gly asp pro ala ala  
 GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

50

phe arg ala leu val ala gln cys leu val cys val pro trp asp  
 TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

60

70

ala arg pro pro pro ala ala pro ser phe arg gln val ser cys  
 GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

80

leu lys glu leu val ala arg val leu gln arg leu cys glu arg  
 CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

90

100

gly ala lys asn val leu ala phe gly phe ala leu leu asp gly  
 GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

110

ala arg gly gly pro pro glu ala phe thr thr ser val arg ser  
 GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

120

FIG. 20A

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                                130
    tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
    TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

                                140
    trp gly leu leu leu arg arg val gly asp asp val leu val his
    TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

                                150

    leu leu ala arg cys ala leu phe val leu val ala pro ser cys
    CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

                                160

    ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala
    GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC

                                170

                                180
    thr gln ala arg pro pro pro his ala ser gly pro arg arg arg
    ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

                                190

    leu gly cys glu arg ala trp asn his ser val arg glu ala gly
    CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

                                200

                                210
    val pro leu gly leu pro ala pro gly ala arg arg arg gly gly
    GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

                                220

    ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly
    AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

                                230

                                240
    ala ala pro glu pro glu arg thr pro val gly gln gly ser trp
    GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

                                250

    ala his pro gly arg thr arg gly pro ser asp arg gly phe cys
    GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

                                260

                                270
    val val ser pro ala arg pro ala glu glu ala thr ser leu glu
    GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG

                                280

    gly ala leu ser gly thr arg his ser his pro ser val gly arg
    GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

                                290

                                300
    gln his his ala gly pro pro ser thr ser arg pro pro arg pro
    CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

                                310

    trp asp thr pro cys pro pro val tyr ala glu thr lys his phe
    TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

                                320

                                330

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FIG. 20B

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                                340
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

                                350
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

                                360

                                370
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

                                380
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

                                390

                                400
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

                                410
val leu leu lys thr his cys pro leu arg ala ala val thr pro
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

                                420

                                430
ala ala gly val cys ala arg glu lys pro gln gly ser val ala
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

                                440
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

                                450

                                460
leu arg gln his ser ser pro trp gln val tyr gly phe val arg
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

                                470
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

                                480

                                490
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

                                500
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

                                510

                                520
met ser val arg asp cys ala trp leu arg arg ser pro gly val
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

                                530
gly cys val pro ala ala glu his arg leu arg glu glu ile leu
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

                                540

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FIG. 20C

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                                550
ala lys phe leu his trp leu met ser val tyr val val glu leu
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

                                560
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

                                570
                                580
arg leu phe phe tyr arg lys ser val trp ser lys leu gln ser
AGG CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC

                                590
ile gly ile arg gln his leu lys arg val gln leu arg glu leu
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

                                600
                                610
ser glu ala glu val arg gln his arg glu ala arg pro ala leu
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

                                620
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

                                630
                                640
pro ile val asn met asp tyr val val gly ala arg thr phe arg
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

                                650
arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

                                660
                                670
phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

                                680
gly ala ser val leu gly leu asp asp ile his arg ala trp arg
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

                                690
                                700
thr phe val leu arg val arg ala gln asp pro pro pro glu leu
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

                                710
tyr phe val lys val asp val thr gly ala tyr asp thr ile pro
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

                                720
                                730
gln asp arg leu thr glu val ile ala ser ile ile lys pro gln
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

                                740
asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

                                750

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FIG. 20D

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his gly his val arg lys ala phe lys ser his val leu arg pro  
 CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC CTA CGT CCA

760  
 val pro gly asp pro ala gly leu his pro leu his ala ala leu  
 GTG CCA GGG GAT CCC GCA GGG CTC CAT CCT CTC CAC GCT GCT CTG

770  
 780  
 gln pro val leu arg arg his gly glu gln ala val cys gly asp  
 CAG CCT GTG CTA CGG CGA CAT GGA GAA CAA GCT GTT TGC GGG GAT

790  
 ser ala gly arg ala ala pro ala phe gly gly OP  
 TCG GCG GGA CGG GCT GCT CCT GCG TTT GGT GGA TGA TTTCTTGTGGT

800  
 807  
 GACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGA  
 GTATGGCTGCGTGGTGAACCTTGCGGAAGACAGTGGTGAACCTTCCCTGTAGAAGACGAGGC  
 CCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCACGGCCTATTCCCCTGGTGCGGCCT  
 GCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTC  
 CATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAA  
 ACTCTTTGGGGTCTTGCGGCTGAAGTGTACAGCCTGTTTCTGGATTTGCAGGTGAACAG  
 CCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCA  
 CGCATGTGTGCTGCAGCTCCCATTTTCATCAGCAAGTTTGGAAGAACCCACATTTTTCCT  
 GCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGG  
 GATGTCGCTGGGGGCCAAGGGCGCCGCCGCGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCT  
 GTGCCACCAAGCATTCCTGCTCAAGCTGACTCGAACCCTGTACCTACGTGCCACTCCT  
 GGGGTCACTCAGGACAGCCCAGACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGAC  
 TGCCCTGGAGGCCGAGCCAACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTG  
 ATGGCCACCCGCCCACAGCCAGGCCGAGAGCAGACACCAGCAGCCCTGTACGCCGGGCT  
 CTACGTCCCAGGGAGGGAGGGGCGGCCACACCCAGGCCCGCACCGCTGGGAGTCTGAGG  
 CCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAG  
 GCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCC  
 CACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTC  
 CACTCCCCACATAGGAATAGTCCATCCCAGATTGCGCCATTGTTACCCCTCGCCCTGCC  
 CTCCTTTGCCTTCCACCCCCACCATCCAGGTGGAGACCTGAGAAGGACCCTGGGAGCTC  
 TGGAATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGAT  
 GGGGTCCCTGTGGGTCAAATTGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATG  
 AGTTTTTCAGTTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 20E

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FIG. 21A

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4321 GGTGTTTTTAAGCCAATNANAAAATTTTTTNATGTTGTTNNNNNNNNNNNNNNNNNNNN  
CCACAAAAATTCGGTTANTNTTTTAAAAAANTACAACAAANNNNNNNNNNNNNNNNNNNN

4381 NNN  
NN

4441 NNN  
NN

4501 NNN  
NN

4561 NNN  
NN

4621 NNN  
NN

4681 NNN  
NN

4741 NNN  
NN

4801 NNN  
NN

4861 NNN  
NN

4921 NNN  
NN

4981 NNN  
NN

5041 NGCCANGRAGGGGGCCAGGTTCCAANTTCCCAACCKTTTWTGGARGGACNGCCCCCAGGG  
NCGGTNCYTCCCCCGGTCCAAGGTTNAAGGGTTGGMAAAAWCCTYCCTGNCGGGGGTCCC

5101 GGGGATRAACAGANTNGGGGGKGGTWGGGTTNAKGGTGGGAACNCCTTNGCGCCTGGAG  
CCCCTAYTTGTCTNANCCCCCMCCAWCCCAANTMCCACCCTTGNGGAANCGSCGGACCTC

5161 AACGTGCAAAGAGGAAATGAAGGGCCTGKGTCAAGGAGCCCAAGTNGGCGGGGRAGTTTG  
TTGCACGTTTCTCCTTTACTTCCCGGACMCAGTTCCTCGGGTTCANCCGCCCCYTCAAAC

5221 CAGGGAGGCACTCCGGGGAGGTCCSGCGTGCCCGTCCAAGGGAGCAATGCGTCCTTCGGG  
GTCCCTCCGTGAGGCCCTCCAGGSCGCACGGGCAGGTTCCCTCGTTACGCAGGAAGCCC

5281 TTCGTCCCCAWGCCGCGTCTACGCGCCTYCCGTCTCCCTTCACGTTCCGGCATTTCGTG  
AAGCAGGGGTWCGGCGCAGATGCGCGGARGGCAGGAGGGGAAGTGCAAGGCCGTAAGCAC

5341 GTGCCCGGAGCCCGACGCCCCGCGTCCGGACCTGGAGGCAGCCCTGGGTCTCCGGATCAG  
CACGGGCCTCGGGCTGCGGGGCGCAGGCCTGGACCTCCGTGCGGACCCAGAGGCCTAGTC

5401 GCCAGCGGCCAAAGGGTCGCCGCACGCACCTGTTCCAGGGCCTCCACATCATGGCCCCCT  
CGGTGCGCCGTTTCCAGCGGCGTGCGTGGACAAGGGTCCCGGAGGTGTAGTACCGGGGA

FIG. 21B

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5461 CCCTCGGGTTACCCACAGCCTAGGCCGGATTTCGACCTCTCTCCGCTGGGGCCCTCGCCT  
GGGAGCCCAATGGGGTGTTCGGATCCGGCCTAAGCTGGAGAGAGGCGACCCCGGGAGCGGA

Sp1

\*\*\*\*\*

5521 GGCGTCCCTGCACCCTGGGAGCGCGAGCGGCGCGGGCGGGGAAGCGCGGCCCATACCC  
CCGCAGGGACGTGGGACCCTCGCGCTCGCCGCGCGCCCGCCCTTCGCGCCGGGTATGGG

5581 CCGGGTCCGCCCCGGAAGCAGCTGCGCTGTTCGGGGCCAGGCCGGGCTCCCAGTGGATTTCGC  
GGCCCAGGCGGGCCTTCGTTCGACGCGACAGCCCCGGTCCGGCCCCGAGGGTCACCTAAGCG

Topo\_II\_cleavage\_site

\*\*\*\*\*

5641 GGGCACAGACGCCCAGGACCGCGCTTCCACGTGGCGGAAGGACTGGGGACCCGGGCACC  
CCCGTGTCTGCGGGTCTTGGCGCGAAGGGTGCACCGCCTTCCTGACCCCTGGGCCCCGTGG

E2F

\*\*\*\*\*

5701 CGTCCTGCCCCCTTCACCTTCCAGCTCCGCTTCTTCCGCGCGGACCCGGCCCCGTCCCGAA  
GCAGGACGGGGAAGTGAAGGTTCGAGGCGAAGAAGGCGCGCCTGGGCGGGGCGAGGGCTT

E

\*\*\*\*

5761 CCCTTCCCAGGTCCCGGGCCAGCCCCCTTCCGGGCCCTCCCAGCCCCCTCCCTTCTTTTC  
GGGAAGGGTCCAGGGCCGGGTTCGGGGAAGGCCCGGGAGGGTTCGGGGAGGGGAAGGAAAAG

Sp1

=====

2F

\*\*\*\*\*

NFkB

\*\*\*\*\*

h

5821 CGCGGCCCCGCCCTCTCCTTCGCGGCGCGAGTTTCAGGCAGCGCTGCGTCTCTGCTGCGCA  
GCGCCGGGGCGGGAGAGGAAGCGCCGCGCTCAAAGTCCGTTCGCGACGCAGGACGACGCGT

5860

ECO47III

5875

FSP1

TRT5'

\*\*\*\*\*&gt;

5881 CGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCCGCGCGCTCCCCGCTGCCGAGCCG  
GCACCCCTTCGGGACCGGGGCCGGTGGGGGCGCTACGGCGCGCGAGGGGCGACGGCTCGGC

5941 TCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTTCGTGCGGC  
ACGCGAGGGACGACGCGTCGGTGATGGCGCTCCACGACGCGACCGGTGCAAGCACGCCG

5953

FSP1

6001 GCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCGCGCGC  
CGGACCCCGGGGTCCCGACCGCCGACCACGTTCGCGCCCCCTGGGCGCCGAAAGGCGCGCG

6061 TGGTGGCCCACTGCGTGGTGTGCGTGGCTGGGACGCACGGCCGCCCCCGCGCCCCCT  
ACCACCGGGTCACGGACCACACGCACGGGACCCTGCGTGGCGGCGGGGGCGGGCGGGGA

NFkB

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FIG. 21C

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*****
6121 CCTTCCGCCAGGTGGGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGG
    GGAAGGCGGTCCACCCGAGGGGCCCCAGCCGAGGCCGACCCCAACTCCCGCCGGCCCC

                                         Topo_II_cleavage_s
                                         :::::::::::::::
                                         NFkB
                                         =====

Intron1
*****>
6181 GGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTGTC
    CCTTGGTTCGCTGTACGCCTCTCGTCGCGTCCGCTGAGTCCCGCAAGGGGGCGTCCACAG

ite
:

6241 CTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCCGCAAGAA
    GACGGACTTCCTCGACCACCGGGCTCACGACGTCTCCGACACGCTCGCGCCGCGCTTCTT

6301 CGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCGCGGGGGCCCCCCCCGAGGCCTT
    GCACGACCGGAAGCCGAAGCGCGACGACCTGCCCCGGGCGCCCCGGGGGGGCTCCGGAA

6361 CACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGG
    GTGGTGGTTCGACGCGTCGATGGACGGGTTGTGCCACTGGCTGCGTGACGCCCCCTCGCC
    ^
    6372
    FSP1

6421 GGCCTGGGGGCTGCTGCTGCGCCGCTGGGCGACGACGTGCTGGTTACCTGCTGGCAGC
    CCGACCCCCGACGACGACGCGGCGCACCCGCTGCTGCACGACCAAGTGGACGACCGTGC

6481 CTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCGCT
    GACGCGCGAGAAACACGACCACCGAGGGTCGACGCGGATGGTCCACACGCCCCGGCGGCGA

6541 GTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAG
    CATGGTCGAGCCGCGACGGTGAGTCCGGGCCGGGGGCGGTGTGCGATCACCTGGGGCTTC

6601 GCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGTCCCCCTGGG
    CGCAGACCCCTACGCTTGCCCGGACCTTGGTATCGCAGTCCCTCCGGCCCCAGGGGGACCC

6661 CCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCC
    GGACGGTCGGGGGCCACGCTCCTCCGCGCCCCCGTCACGGTCGGCTTCAGACGGCAACGG

6721 CAAGAGGCCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCCGTTGGGCAGGGGTC
    GTTCTCCGGGTCCGCACCGCGACGGGACTCGGCCTCGCCTGCGGGCAACCCGTCCCCAG

6781 CTGGGCCCCACCGGGCAGGACGCGTGACCGAGTGACCGTGTTTCTGTGTGGTGTACCC
    GACCCGGGTGGGCCCGTCTGCGCACCTGGCTCACTGGCACCAAGACACACCACAGTGG

6841 TGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTC
    ACGGTCTGGGCGGCTTCTTCGGTGGAGAAACCTCCACGCGAGAGACCGTGCGCGGTGAG

6901 CCACCCATCCGTGGGCGGCCAGCACCAACGCGGGCCCCCATCCACATCGCGGCCACCACG
    GGTGGGTAGGCACCCGCGGTCGTGGTGCGCCCGGGGGGTAGGTGTAGCGCCGGTGGTGC

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FIG. 21D

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6961 TCCCTGGGACACGCCTTGTCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTC  
AGGGACCTGTGCGGAACAGGGGGCCACATGCGGCTCTGGTTCGTGAAGGAGATGAGGAG

7021 AGGCGACAAGGAGCAGCTGCGGCCCTCCTTCTACTCAGCTCTCTGAGGCCCAGCCTGAC  
TCCGCTGTTCCTCGTCGACGCCGGGAGGAAGGATGAGTCGAGAGACTCCGGGTTCGGA

7081 TGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCAGGCCCTGGATGCCAGGGAC  
ACCGCGAGCCTCCGAGCACCTCTGGTAGAAAGACCCAAGTCCGGGACCTACGGTCCCTG

7141 TCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCTGTTTCTGGA  
AGGGGCGTCCAACGGGGCGGACGGGGTCGCGATGACCGTTACGCCGGGGACAAAGACCT

7167  
ECO47III

7201 GCTGCTTGGGAACCACGCGCAGTGGCCCTACGGGGTGCTCCTCAAGACGCACTGCCCCGT  
CGACGAACCTTGGTGCGCGTCACGGGGATGCCCCACGAGGAGTTCTGCGTGACGGGCGA

7261 GCGAGCTGCGGTACCCACGACGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGT  
CGCTCGACGCCAGTGGGGTTCGTGCGCCACAGACACGGGCCCTCTTCGGGGTCCCGAGACA

7321 GGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTGCTTGGTGCAGCTGCTCCGCCAGCA  
CCGCCGGGGGCTCCTCCTCCTGTGTCTGGGGGCAGCGGACCACGTGACGAGGCGGTCTGT

7381 CAGCAGCCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCC  
GTCGTGCGGGACCGTCCACATGCCGAAGCACGCCCGGACGGACGCGGCCGACCCAGGGGG

7441 AGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCTCAGGAACACCAAGAAGTTCAT  
TCCGGAGACCCCGAGGTCCGTGTTGCTTGCGGCGAAGGAGTCCTTGTGGTTCTTCAAGTA

7501 CTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCG  
GAGGGACCCCTTCGTACGGTTCGAGAGCGACGTCTCGACTGCACCTTCTACTCGCACGC

\*\*\*\*\*

7561 GGA CTGCGCTTGGCTGCGCAGGAGCCAGGTGAGGAGGTGGTGGCCGTGAGAGGCCAGG  
CCTGACGCGAACCAGCGCTCCTCGGGTCCACTCCTCCACCACCGGCAGCTCCCGGGTCC

7575  
FSP1

Intron2

\*\*\*\*\*

7621 CCCCAGAGCTGAATGCAGTAGGGGCTCAGAAAAGGGGCGAGGAGCCCTGGTCTCCT  
GGGGTCTCGACTTACGTTCATCCCCAGTCTTTTCCCCCGTCCGTCTCGGGACCAGGAGGA

\*\*\*\*\*

7681 GTCTCCATCGTCACGTGGGCACACGTGGCTTTTCGCTCAGGACGTGAGTGACACGGTG  
CAGAGGTAGCAGTGCACCCGTGTGCACCGAAAAGCGAGTCCTGCAGCTCACCTGTGCCAC

\*\*>

7741 ATCGAGGTGCACTCTAGAGGATCCCCGGGTACCGAGCTCGAATTCGTAATCATGGTCATA  
TAGCTCCAGCTGAGATCTCCTAGGGGCCCATGGCTCGAGCTTAAGCATTAGTACCAGTAT

7747  
SAL1

FIG. 21E

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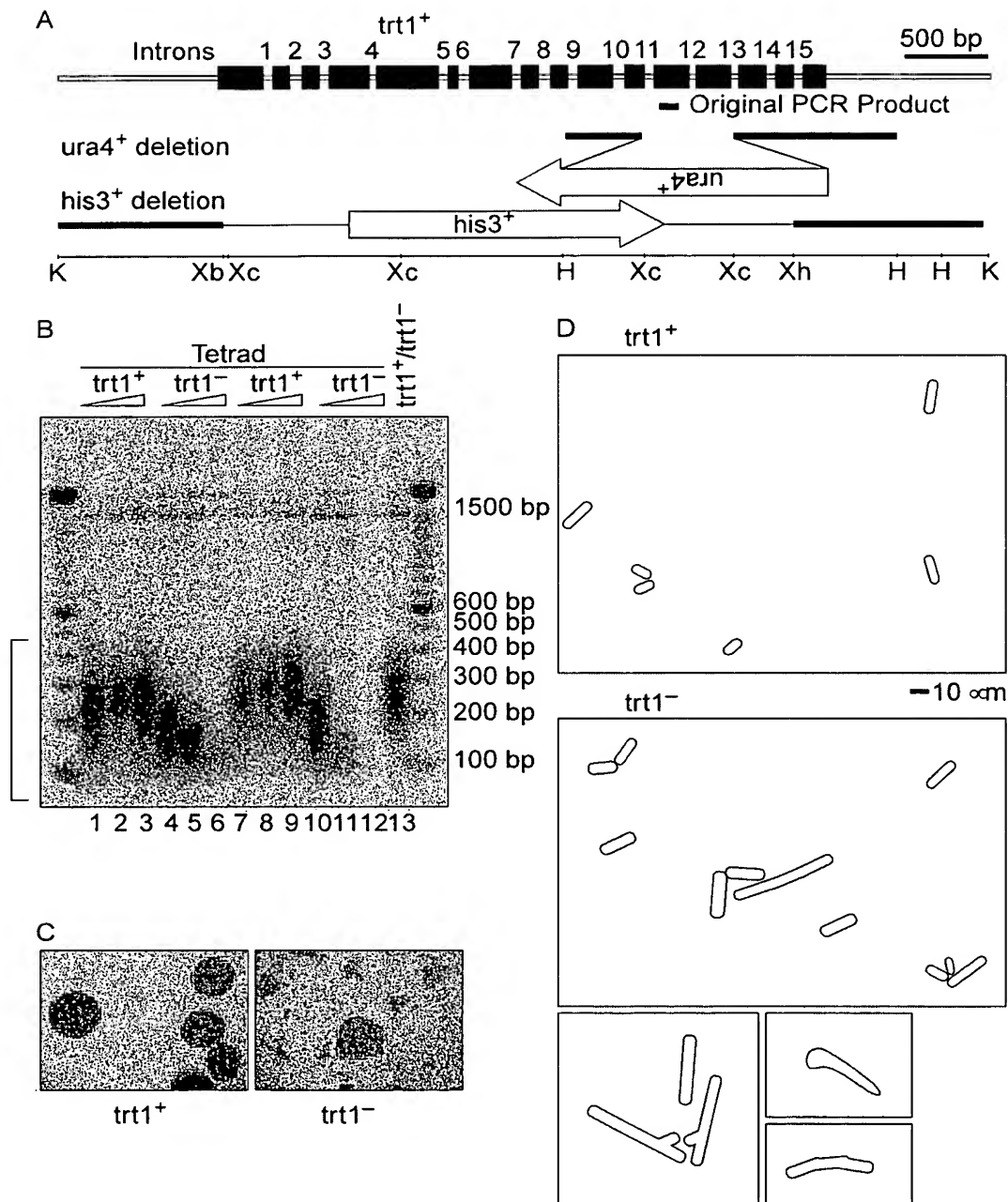


FIG. 22



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gccaagttcctgcactggctgatgagtgtgtacgtcgtcgagctgctcaggtctttcttt  
tatgtcacggagaccacgtttcaaaagaacaggctctttttctaccggaagagtgtctgg  
agcaagttgcaaagcattggaatcagacagcacttgaagaggggtgcagctgcgggacgtg  
tcggaagcagaggtcaggcagcatcggaagccaggcccgccctgctgacgtccagactc  
cgcttcatccccaaagcctgacgggctgcggccgatttgtgaacatggactacgtcgtggga  
gccagaacgttccgcagagaaaagagggccgagcgtctcacctcgaggggtgaaggcactg  
ttcagcgtgctcaactacgagcgggcgcg

FIG. 23

TCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAG  
ACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCC  
AGCAGTGGCCTCTTCGACGTCTTCTACGCTTCATGTGCCACCACGCCGTGCGCATC  
AGGGGCAAGTC

FIG. 24

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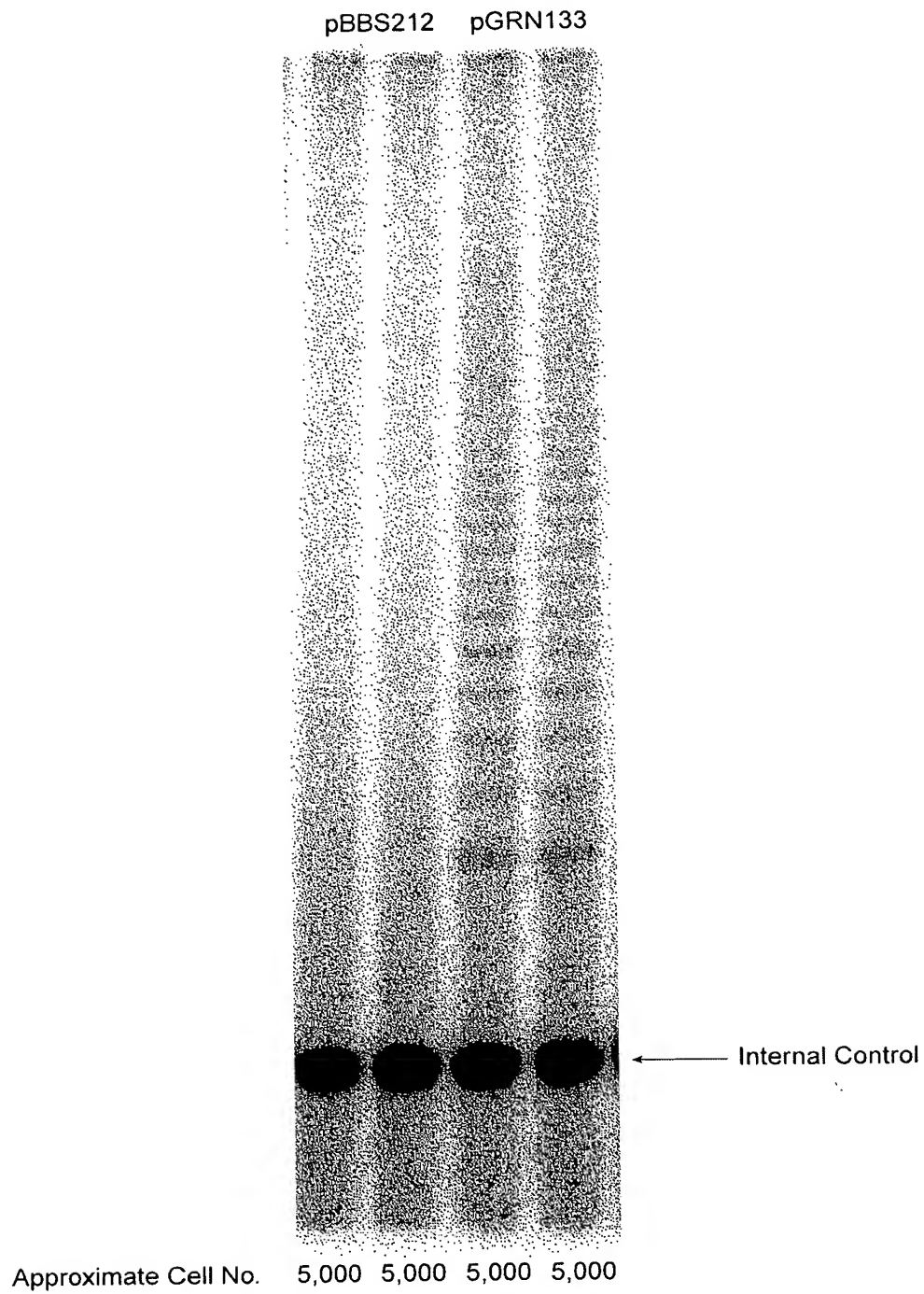


FIG. 25

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